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<110>  Li et al.

<120>  G-Protein Receptor HTNAD29

<130>  PF191D1C1

<150>  US95/07288
<151>  1995-06-06

<150>  08/468,534
<151>  1995-06-06

<150>  09/399,095
<151>  1999-09-20

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<170>  PatentIn Version 3.1

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<213>  Homo sapiens

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<222>  (523)..(1533)
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catggaagga aaggaatttt aaaaggaaat accaatctct gtgcaaacaa agccttgtat     120

attcatgttt gcaccaatct actgtgagat ttatgaagaa aaacaaattg cggacaactc     180

tctatgtaca cttacaaatg cctcagttga tgcttgtggg ctgtttgtca gcgttctgtg     240

ataatgaaca catggacttc tgtttattaa attcagttga ccccttttagc caattgccag     300

gagcctggat ttttacttcc aactgctgat atctgtgtaa aaattgatct acatccaccc     360

tttaaaagca ttgatgaatt aattagaact ttagacaaca agaaaaattg aaaagaattc     420

tcagtaaaag cgaattcgat gttcaaaaca aactacaaag agacaagact tctctgttta     480

ctttctaaga actaatataa ttgctacctt aaaaaggaaa aa atg aac agc aca     534
                                                Met Asn Ser Thr
                                                  1

tgt att gaa gaa cag cat gac ctg gat cac tat ttg ttt ccc att gtt     582
Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu Phe Pro Ile Val
  5                10                  15                  20

tac atc ttt gtg att ata gtc agc att cca gcc aat att gga tct ctg     630
Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn Ile Gly Ser Leu
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                  25                    30                         35

tgt gtg tct ttc ctg caa ccc aag aag gaa agt gaa cta gga att tac        678
Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu Leu Gly Ile Tyr
                40                    45                    50

ctc ttc agt ttg tca cta tca gat tta ctc tat gca tta act ctc cct        726
Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala Leu Thr Leu Pro
                55                    60                    65

tta tgg att gat tat act tgg aat aaa gac aac tgg act ttc tct cct        774
Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp Thr Phe Ser Pro
        70                    75                    80

gcc ttg tgc aaa ggg agt gct ttt ctc atg tac atg aag ttt tac agc       822
Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met Lys Phe Tyr Ser
85                    90                    95                   100

agc aca gca ttc ctc acc tgc att gcc gtt gat cgg tat ttg gct gtt       870
Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg Tyr Leu Ala Val
                     105                   110                   115

gtc tac cct ttg aag ttt ttt ttc cta agg aca aga aga att gca ctc       918
Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg Arg Ile Ala Leu
                     120                   125                   130

atg gtc agc ctg tcc atc tgg ata ttg gaa acc atc ttc aat gct gtc       966
Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile Phe Asn Ala Val
                     135                   140                   145

atg ttg tgg gaa gat gaa aca gtt gtt gaa tat tgc gat gcc gaa aag      1014
Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys Asp Ala Glu Lys
150                   155                   160

tct aat ttt act tta tgc tat gac aaa tac cct tta gag aaa tgg caa      1062
Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu Glu Lys Trp Gln
165                   170                   175                   180

atc aac ctc aac ttg ttc agg acg tgt aca ggc tat gca ata cct ttg      1110
Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr Ala Ile Pro Leu
                     185                   190                   195

gtc acc atc ctg atc tgt aac cgg aaa gtc tac caa gct gtg cgg cac      1158
Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln Ala Val Arg His
                     200                   205                   210

aat aaa gcc acg gaa aac aag gaa aag aag aga atc ata aaa cta ctt      1206
Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile Ile Lys Leu Leu
                     215                   220                   225

gtc agc atc aca gtt act ttt gtc tta tgc ttt act ccc ttt cat gtg      1254
Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr Pro Phe His Val
        230                   235                   240

atg ttg ctg att cgc tgc att tta gag cat gct gtg aac ttc gaa gac      1302
Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val Asn Phe Glu Asp
245                   250                   255                   260

cac agc aat tct ggg aag cga act tac aca atg tat aga atc acg gtt      1350

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His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr Arg Ile Thr Val
                265                 270                 275

gca tta aca agt tta aat tgt gtt gct gat cca att ctg tac tgt ttt      1398
Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Phe
            280                 285                 290

gtt acc gaa aca gga aga tat gat atg tgg aat ata tta aaa ttc tgc      1446
Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile Leu Lys Phe Cys
            295                 300                 305

act ggg agg tgt aat aca tca caa aga caa aga aaa cgc ata ctt tct      1494
Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys Arg Ile Leu Ser
            310                 315                 320

gtg tct aca aaa gat act atg gaa tta gag gtc ctt gag tagaaccaag      1543
Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu Glu
325                 330                 335

gatgttttga agggaaggga agtttaagtt atgcattatt atatcatcaa gattacattt      1603

tgaaaaggaa atctagcatg tgaggggact aagtgttctc agagtgatgt tttaatccag      1663

tccaataaaa atatcttaaa actgcattgt acagctccct ccctgcgttt tattaaatga      1723

tgtatattaa acaaagatca atattttctt                                      1753


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<213>   Homo sapiens

<400>   2

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
1               5                   10                  15


Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
                20                  25                  30


Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu
            35                  40                  45


Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
        50                  55                  60


Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
65                  70                  75                  80


Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
                85                  90                  95
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3

```
Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
            100                 105                 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Leu Arg Thr Arg
        115                 120                 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
    130                 135                 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
145                 150                 155                 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
            165                 170                 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
        180                 185                 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
        195                 200                 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
    210                 215                 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr
225                 230                 235                 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val
            245                 250                 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr
            260                 265                 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
        275                 280                 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile
        290                 295                 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys
305                 310                 315                 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu
            325                 330                 335
```

4

Glu

```
Asp Ser Ser His Met Asp Ser Glu Phe Arg Tyr Thr Leu Phe Pro Ile
1               5                   10                  15

Val Tyr Ser Ile Ile Phe Val Leu Gly Val Ile Ala Asn Gly Tyr Val
            20                  25                  30

Leu Trp Val Phe Ala Arg Leu Tyr Pro Cys Lys Lys Phe Asn Glu Ile
            35                  40                  45

Lys Ile Phe Met Val Asn Leu Thr Met Ala Asp Met Leu Phe Leu Ile
        50                  55                  60

Thr Leu Pro Leu Trp Ile Val Tyr Tyr Gln Asn Gln Gly Asn Trp Ile
65                  70                  75                  80

Leu Pro Lys Phe Leu Cys Asn Val Ala Gly Cys Leu Phe Phe Ile Asn
                85                  90                  95

Thr Tyr Cys Ser Val Ala Phe Leu Gly Val Ile Thr Tyr Asn Arg Phe
            100                 105                 110

Gln Ala Val Thr Arg Pro Ile Lys Thr Ala Gln Ala Asn Thr Arg Lys
            115                 120                 125

Arg Gly Ile Ser Leu Ser Leu Val Ile Trp Val Ala Ile Val Gly Ala
        130                 135                 140

Ala Ser Tyr Phe Leu Ile Leu Asp Ser Thr Asn Thr Val Pro Asp Ser
145                 150                 155                 160

Ala Gly Ser Gly Asn Val Thr Arg Cys Phe Glu His Tyr Glu Lys Gly
                165                 170                 175

Ser Val Pro Val Leu Ile Ile His Ile Phe Ile Val Phe Ser Phe Phe
            180                 185                 190
```

```
Leu Val Phe Leu Ile Ile Leu Phe Cys Asn Leu Val Ile Ile Arg Thr
        195                 200                 205

Leu Leu Met Gln Pro Val Gln Gln Gln Arg Asn Ala Glu Val Thr Gly
    210                 215                 220

Arg Ala Leu Trp Met Val Cys Thr Val Leu Ala Val Phe Ile Ile Cys
225                 230                 235                 240

Phe Val Pro His His Val Val Gln Leu Pro Trp Thr Leu Ala Glu Leu
            245                 250                 255

Gly Phe Gln Asp Ser Lys Phe His Gln Ala Ile Asn Asp Ala His Gln
        260                 265                 270

Val Thr Leu Cys Leu Leu Ser Thr Asn Cys Val Leu Asp Pro Val Ile
        275                 280                 285

Tyr Cys Phe Leu Thr Lys Lys Phe Arg Lys His Leu Thr Glu Lys Phe
        290                 295                 300

Tyr Ser Met Arg Ser Ser Arg Lys Cys Ser Arg Ala Thr Thr Asp Thr
305                 310                 315                 320

Val Thr Glu Val Val Val Pro
            325


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<212>   DNA
<213>   Artificial sequence

<220>
<223>   Contains an EcoRI restriction enzyme site

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cgaattcctc catgaacagc acatgtatt                                        29


<210>   5
<211>   29
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Contains complementary sequences to a HindIII site

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cggaagcttc gtcaaggacc tctaattcc                                        29
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<211>  34
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Contains a HindIII site

<400>  6
gtccaagctt gccaccatga acagcacatg tatt                            34


<210>  7
<211>  61
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Contains complementary sequences to an XhoI site,
translation stop codon, and an HA tag

<400>  7
ctagctcgag tcaagcgtag tctgggacgt cgtatgggta gcaaggacct ctaattccat   60

a                                                                 61


<210>  8
<211>  30
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Contains a BamHI restriction enzyme site followed by 4
nucleotides resembling an efficient signal for the initiation
of translation in eukaryotic cells

<400>  8
cgggatccct ccatgaacag cacatgtatt                                  30


<210>  9
<211>  32
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Contains the cleavage site for the restriction
endonuclease BamHI

<400>  9
cgggatcccg ctcaaggacc tctaattcca ta                               32
```